**Amendments to the Claims:**

This listing of claims will replace all prior versions and listings of claims in the application:

**Listing of Claims:**

1) (Original) A method for the detection of methylated DNA against a background of unmethylated DNA is hereby characterized in that

a) the double strands of the DNA to be investigated are separated and then reassociated with the formation of hemimethylated double strands,

b) the hemimethylated positions that are formed in step a) are converted into fully methylated positions by means of an enzyme,

c) the methylated DNA is analyzed.

2) (Original) The method according to claim 1, further characterized in that DNA from body fluids is investigated.

3) (Original) The method according to claim 2, further characterized in that DNA from serum is investigated.

4) (Currently amended) The method according to ~~at least one of claims~~ claim 1 ~~to 3~~, further characterized in that the DNA of step a) is fragmented.

5) (Currently amended) The method according to ~~at least one of claims~~ claim 1 ~~to 4~~, further characterized in that a maintenance methyltransferase is used in step b).

6) (Original) The method according to claim 5, further characterized in that DNMT1 is used as the maintenance methyltransferase.

7) (Currently amended) The method according to ~~at least one of claims~~ claim 1 ~~to 6~~, further characterized in that steps a) and b) are repeated once more or several times.

8) (Currently amended) The method according to ~~at least one of claims~~ claim 1 ~~to 7~~, further characterized in that a heat-stable methyltransferase is used.

9) (Currently amended) The method according to ~~at least one of claims~~ claim 1 ~~to 8~~, further characterized in that the DNA in step c) is first converted by means of a bisulfite reagent or enzymatically.

10) (Original) The method according to claim 9, further characterized in that the converted DNA is analyzed by means of one of the following methods: MSP, heavy methyl, MsSNuPE, methyl light.

11) (Currently amended) Use of ~~one of~~ the ~~methods according to at least one~~ method of _any of_ claims 1-10 for the diagnosis or prognosis of cancer disorders or other diseases associated with a change in the cytosine methylation status, for predicting undesired drug effects, for establishing a specific drug therapy, for monitoring the success of a drug therapy, for distinguishing cell

types or tissues and for investigating cell differentiation.

12) (Original) A method for the detection of unmethylated DNA against a background of

methylated DNA is hereby characterized in that

a) the double strands of the DNA to be investigated are separated and then reassociated

with the formation of hemimethylated double strands,

b) the hemimethylated positions that are formed in step a) are converted into

unmethylated positions by means of an enzyme,

c) the unmethylated DNA is analyzed.